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VSP HOMOLOGIES

	1	5	10	15	20	25	30
VSP-b	RSSEYVK	CASFR	AYEA	INIR	AEK	LIPE	EECY
VSP-a	RTPEYVK	CASWR	AYEA	INIR	AEK	LIPE	EECY
T.phos		LKCTT	WRFFV	ETNNL	SPWKT	IP	EECA
Ph.vulg	SDTEY	RCASW	RAYEA	QNI	EEET	IP	QQCY
Ar.VSP		PNCRS	WHIG	FETSN	MIN	FEETV	PANCK
Ar.1A-1	SINYP	PNCRS	WHIG	VETSN	MIN	FEETV	PANCK
Ar17A-1	SINYA	NCRS	WHIG	VETSN	MIN	FEED	V PANCK
	31	35	40	45	50	55	
VSP-b	EPIKEY	INGE	QFRSE	SKTYN	QQA	FFY	ASE
VSP-a	EATKEY	INGE	QFRSE	SKTYN	QQA	FFY	ARD
T.phos	OYVKEY	MVSG	PGYK	MEID	RVSD	EAGE	YAKS
Ph.vulg	DATANY	IEGG	QYRS	DSKTYN	QGI	YEF	FARD
Ar.VSP	AYVED	YLITS	KQY	YDSK	IVN	KEAY	FYAKG
Ar.1A-1	AYVED	YLITS	KQY	YDSK	IVN	KEAY	FYAKG
Ar17A-1	OYVED	YLITS	KQY	YDSK	IVN	KEAY	FYAKG
	60	65	70	75	80	85	
VSP-b	REV	HHND	IFIF	GI	DNIV	LSNI	PYYEK
VSP-a	LEV	HPKD	TFV	SI	DNIV	LSNI	PYYKK
T.phos	VDE	GDD	GRD	WIF	EDV	DEIL	LSNLP
Ph.vulg	RHV	HEND	VILE	NID	GI	ALSNI	PYYSQ
Ar.VSP	EAK	NDI	INV	WIF	EDD	ETL	ESSIP
Ar.1A-1	EAK	NDI	INV	WIF	EDD	ETL	ESSIP
Ar17A-1	EAK	NDI	INV	WIF	EDD	ETL	ESSIP
	90	95	100	105	110	115	
VSP-b	YGVEE	EFNET	LYDE	WV	NKGD	APAL	PETLKN
VSP-a	YGVEE	EFNET	LYDE	WV	NKGN	APAL	PETLKN
T.phos	YGLE	VED	DDVE	FQK	WV	ENG	TAPAL
Ph.vulg	YGSE	KED	SERY	DEE	FV	NKGE	APAL
Ar.VSP	YGI	ENT	AAG	AYW	SW	LYS	CE
Ar.1A-1	YGI	ENT	AAG	AYW	SW	LYS	CE
Ar17A-1	YGI	ENT	AAG	AYW	SW	LYS	CE

TO FIG. 1B.

FIG. 1A.



APPROVED
O.G. FIG.
CLASS. SYMBOL

Title: Compositions and Methods for Altering Amino Acid Content of Proteins
Inventor(s): Rao *et al.*
Application No: 09/478,598
Atty Dkt N : 5718-16A (35718/193734)

FROM FIG. 1A.

	120	125	130	135	140	145
VSP-b	Y	N	K	L	S	L
VSP-a	Y	N	K	L	V	S
T.phos	Y	Q	E	V	L	K
Ph.vulg	Y	N	K	L	V	S
Ar.VSP	Y	E	N	L	L	E
Ar.1A-1	Y	E	N	L	L	E
Ar17A-1	Y	C	N	I	I	E
	150	155	160	165	170	175
VSP-b	K	A	G	E	H	T
VSP-a	K	A	G	Y	H	T
T.phos	N	A	G	E	H	D
Ph.vulg	K	A	G	Y	N	T
Ar.VSP	A	V	G	V	I	K
Ar.1A-1	A	V	G	V	I	K
Ar17A-1	A	A	G	V	I	Y
	180	185	190	195	200	205
VSP-b	R	E	N	L	R	Q
VSP-a	R	E	K	L	I	R
T.phos	R	N	A	M	Y	E
Ph.vulg	R	A	K	L	V	Q
Ar.VSP	R	N	S	L	V	R
Ar.1A-1	R	N	S	L	V	K
Ar17A-1	R	N	K	L	V	K
	210	218				
VSP-b	R	T	E	K	L	P
VSP-a	R	T	E	K	L	P
T.phos	R	S	E	K	L	P
Ph.vulg	R	S	E	K	L	P
Ar.VSP	R	V	E	K	L	P
Ar.1A-1	R	V	E	K	L	P
Ar17A-1	R	V	E	K	L	P

FIG. 1B.



APPROVED D.G. F.B.

Title: Compositions and Methods for Altering Amino Acid Content of

Proteins

Inventor(s): Rao *et al.*

Application No: 09/478,598

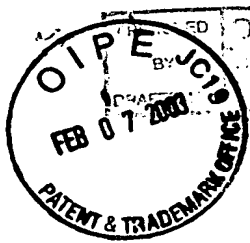
Atty Dkt N : 5718-16A (35718/193734)

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PROPOSED VSP β METHIONINE-ENRICHED VARIANTS

	1	5	10	15	20	25	30
VSPβ	R	S	S	E	V	K	C
VSPβ-Met10		M			M		M
VSPβ-Met20		M			M		M
VSPβ-Met30		M			M	M	M
	31	35	40	45	50	55	60
VSPβ	E	P	T	K	D	Y	I
VSPβ-Met10			M		M		M
VSPβ-Met20	M		M		M		M
VSPβ-Met30	M		M		M		M
	61	65	70	75	80	85	90
VSPβ	E	V	H	N	D	I	F
VSPβ-Met10	M		M		M		
VSPβ-Met20	M	M	M		M		M
VSPβ-Met30	M	M	M		M		M
	91	95	100	105	110	115	120
VSPβ	E	E	F	N	E	T	L
VSPβ-Met10							
VSPβ-Met20			M		M		
VSPβ-Met30		M	M		M		
	121	125	130	135	140	145	150
VSPβ	L	S	L	G	F	K	I
VSPβ-Met10	M		M		M		M
VSPβ-Met20	M		M	M	M		M
VSPβ-Met30	M		M	M	M	M	M
	151	155	160	165	170	175	180
VSPβ	H	T	W	E	Q	L	I
VSPβ-Met10						M	M
VSPβ-Met20				M	M	M	M
VSPβ-Met30			M	MM	M	M	M
	181	185	190	195	200	205	210
VSPβ	R	Q	G	Y	R	I	V
VSPβ-Met10			M			M	
VSPβ-Met20			M		M	M	M
VSPβ-Met30			M		M	M	M
	211	215	218				
VSPβ	P	N	P	M	Y	I	E
VSPβ-Met10		M	M				
VSPβ-Met20		M	M				
VSPβ-Met30		M	M				

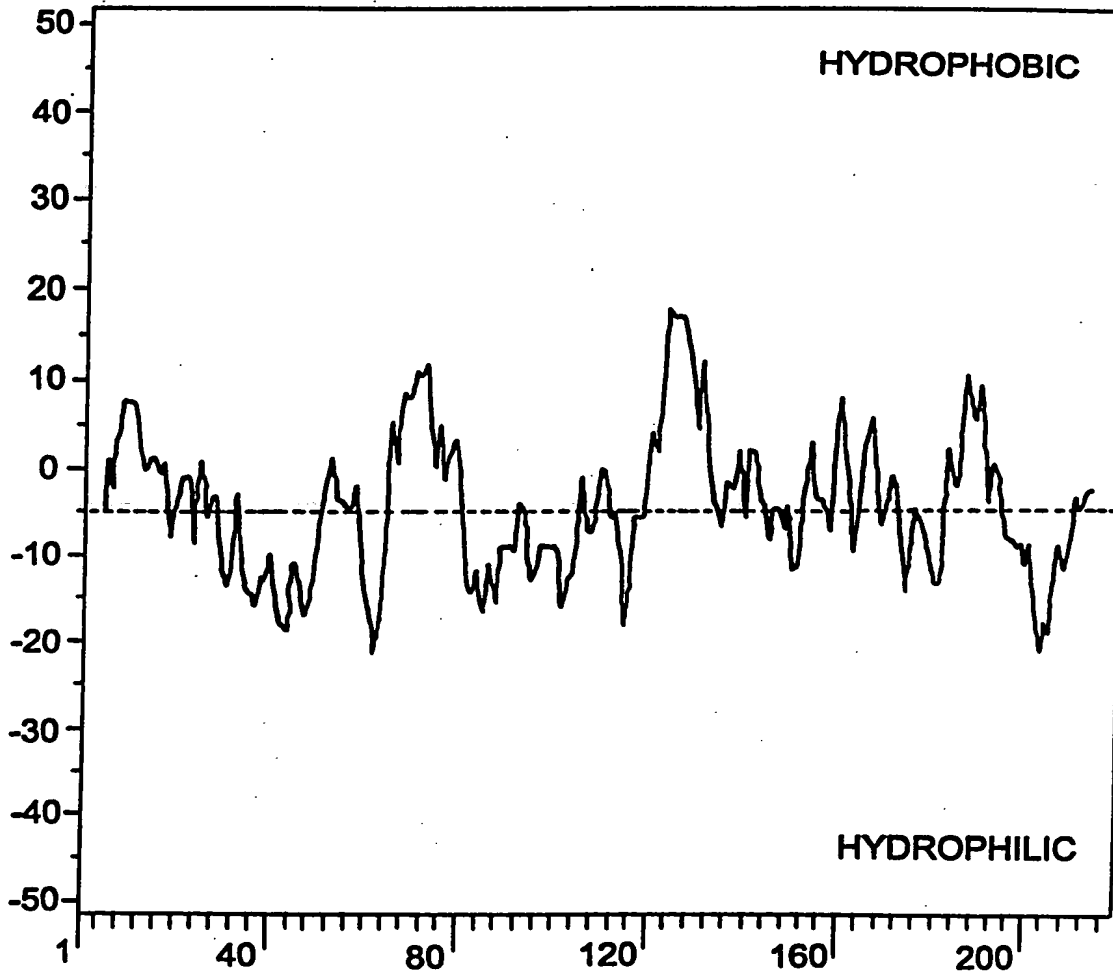
FIG. 2.



Title: Compositions and Methods for Altering Amin Acid Content of
Proteins
Inventor(s): Rao *et al.*
Application No: 09/478,598
Atty Dkt No: 5718-16A (35718/193734)

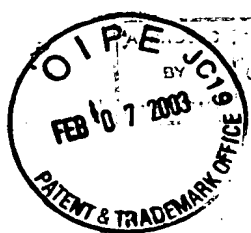
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HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPB.
TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPB FROM AMINO ACID 1 TO AMINO ACID 218.
COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-4.95).

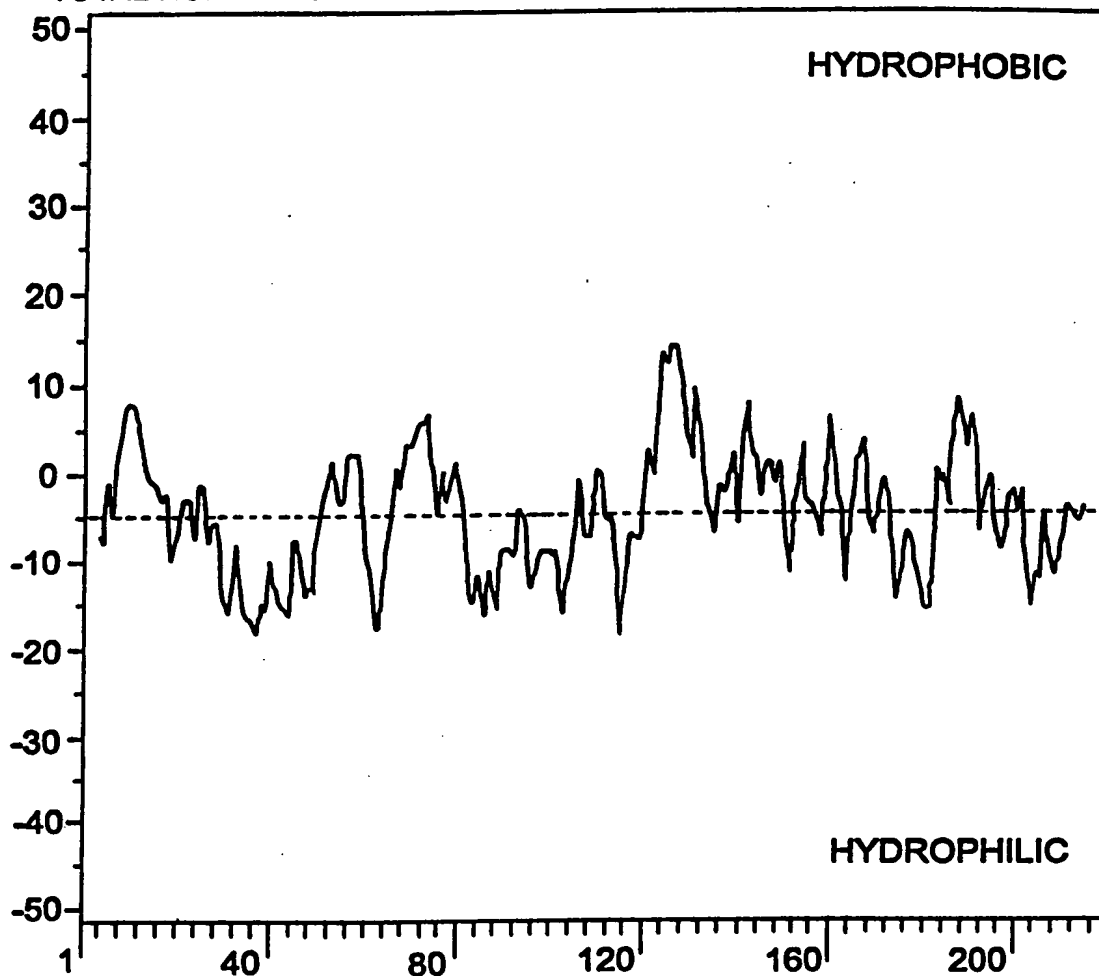
FIG. 3A.



Title: Compositions and Methods for Altering Amino Acid Content of
Inventor(s): Rao *et al.*
Application No: 09/478,598
Atty Dkt No: 5718-16A (35718/193734)

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HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM10.
TOTAL NUMBER OF AMINO ACIDS IS: 218



HYDROPATHIC INDEX OF VSPM1 FROM AMINO ACID 1 TO AMINO ACID 218.
COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=5.52).

FIG. 3B.

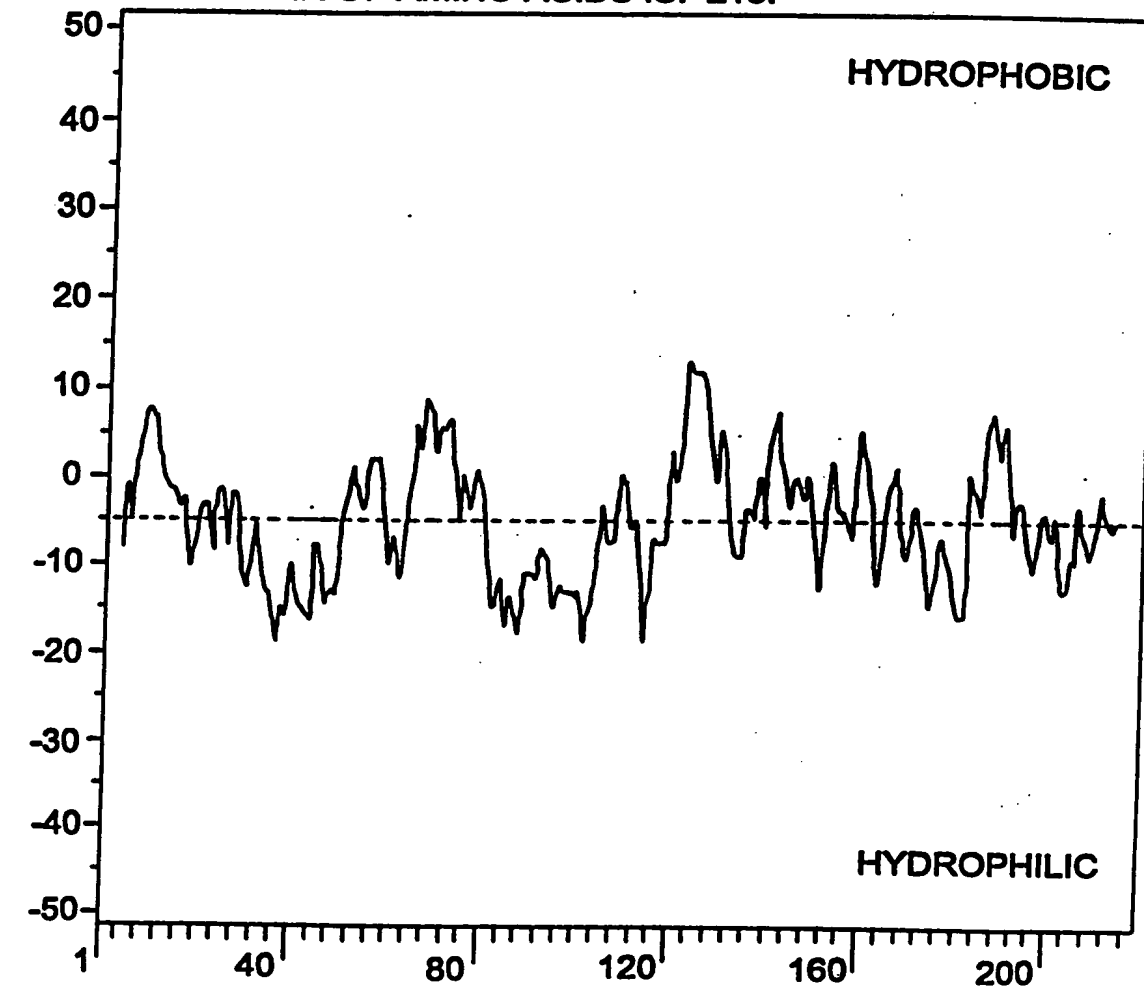


APPROVED	O.G. FIG.
FEB 07 2003	CLASS
CRAFTSMAN	SUBCLASS

Title: Compositions and Methods for Altering Amino Acid Content of
Inventor(s): Rao *et al.*
Application No: 09/478,598
Atty Dkt No: 5718-16A (35718/193734)

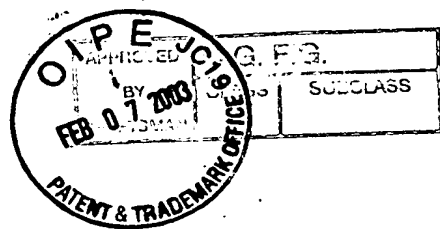
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HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM20.
TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPM20 FROM AMINO ACID 1 AMINO ACID 210.
COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-5.68).

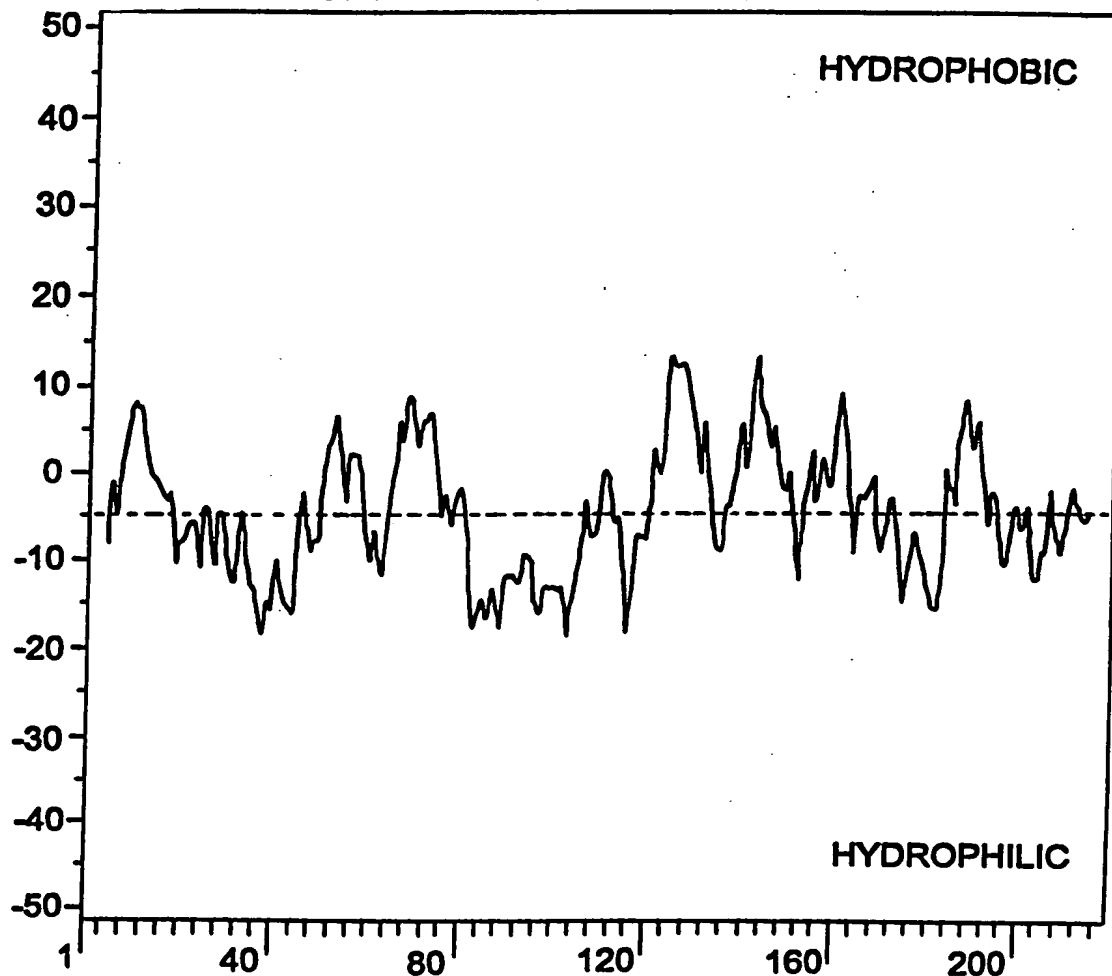
FIG. 3C.



Title: Compositions and Methods for Altering Amino Acid Content of
Proteins
Inv(s): Rao *et al.*
Application No: 09/478,598
Atty Dkt No: 5718-16A (35718/193734)

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HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM30.
TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPM30 FROM AMINO ACID 1 TO AMINO ACID 218.
COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-5.31).

FIG. 3D.



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VSP β -met10 sequence

SfiI

1 GGCCCAGCCGGCCAGATCTTCGGAGATGAAATGCGCTAGCTTTAGGCTTGCTGTGGAAGC 60
CCGGGTTCGGCCGGTCTAGAAGCCTCTACTTTACGCGATCGAAATCCGAACGACACCTTCG

61 ACACAACATGCGAGCCTTTAAAACCATTCCTGAAGAGTGCATGGAACCAACAAAGGACTA 120
TGTGTTGTACGCTCGGAAATTTTGTAAGGACTTCTCACGTACCTTGGTTGTTTCCTGAT

121 CATGAATGGCGAACAATTTTGAATGGACTCTAAAACAGTTAACCAACAGGCCTTCTTTTA 180
GTACTTACCGCTTGTTAAAGCTTACCTGAGATTTTGTCAATTGGTTGTCCGGAAGAAAAT

181 TGCTAGTGAAATGGAAATGCATCACAACGACATGTTTATATTCCGGCATGGATAACACCAT 240
ACGATCACTTTACCTTTACGTAGTGTTGCTGTACAAATATAAGCCGTACCTATTGTGGTA

241 GCTCTCTAATATCCCATACTATGAAAAACATGGATATGGGGTGGAGGAATTTAATGAAAC 300
CGAGAGATTATAGGGTATGATACTTTTTGTACCTATACCCACCTCCTTAAATTACTTTG

301 CTTATATGATGAATGGGTAAACAAGGGCGACGCACCGGCATTGCCAGAGACTCTTAAAAA 360
GAATATACTACTTACCCAATTGTTCCCGCTGCGTGGCCGTAACGGTCTCTGAGAATTTTT

361 TTACAACAAGCTGATGTCCCTTGGCTTCAAGATGGTATTCTTGTCAGGAAGGTACCTTGA 420
AATGTTGTTTCGACTACAGGGAACCGAAGTTCTACCATAAGAACAGTCCTTCCATGGAAT

421 CAAAATGGCCGTAACAGAAGCAAACCTAATGAAGGCTGGCTTCCACACATGGGAGCAGTT 480
GTTTTACCGGCATTGTCTTCGTTTGGATTACTTCCGACCGAAGGTGTGTACCTCGTCAA

481 AATTCTCAAGGATCCACATCTTATGACTCCAAATGCACCTTTCATACAAATCAGCAATGAG 540
TTAAGAGTTCCTAGGTGTAGAATACTGAGGTTTACGTGAAAGTATGTTTAGTCGTTACTC

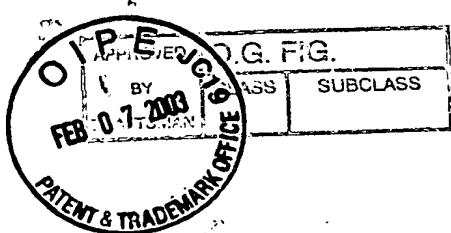
541 AGAGAATATGTTGAGGCAGGGATACAGAATTGTTGGAATGATTGGTGATCAATGGAGCGA 600
TCTCTTATACAACTCCGTCCCTATGTCTTAACAACCTTACTAACCCTAGTTACCTCGCT

601 TCTGCTTGGAGACCACATGGGCGAATCTAGAACCTTTAAGCTTCCTAATCCCATGTACTA 660
AGACGAACCTCTGGTGTACCCGCTTAGATCTTGGAATTCTGAAGGATTAGGGTACATGAT

661 CATGGAGGCGGCCGC 675
GTACCTCCGCGGCG

NotI

Fig. 4



COLONY LIFT ASSAY TO DETECT PROTEIN-PROTEIN INTERACTIONS

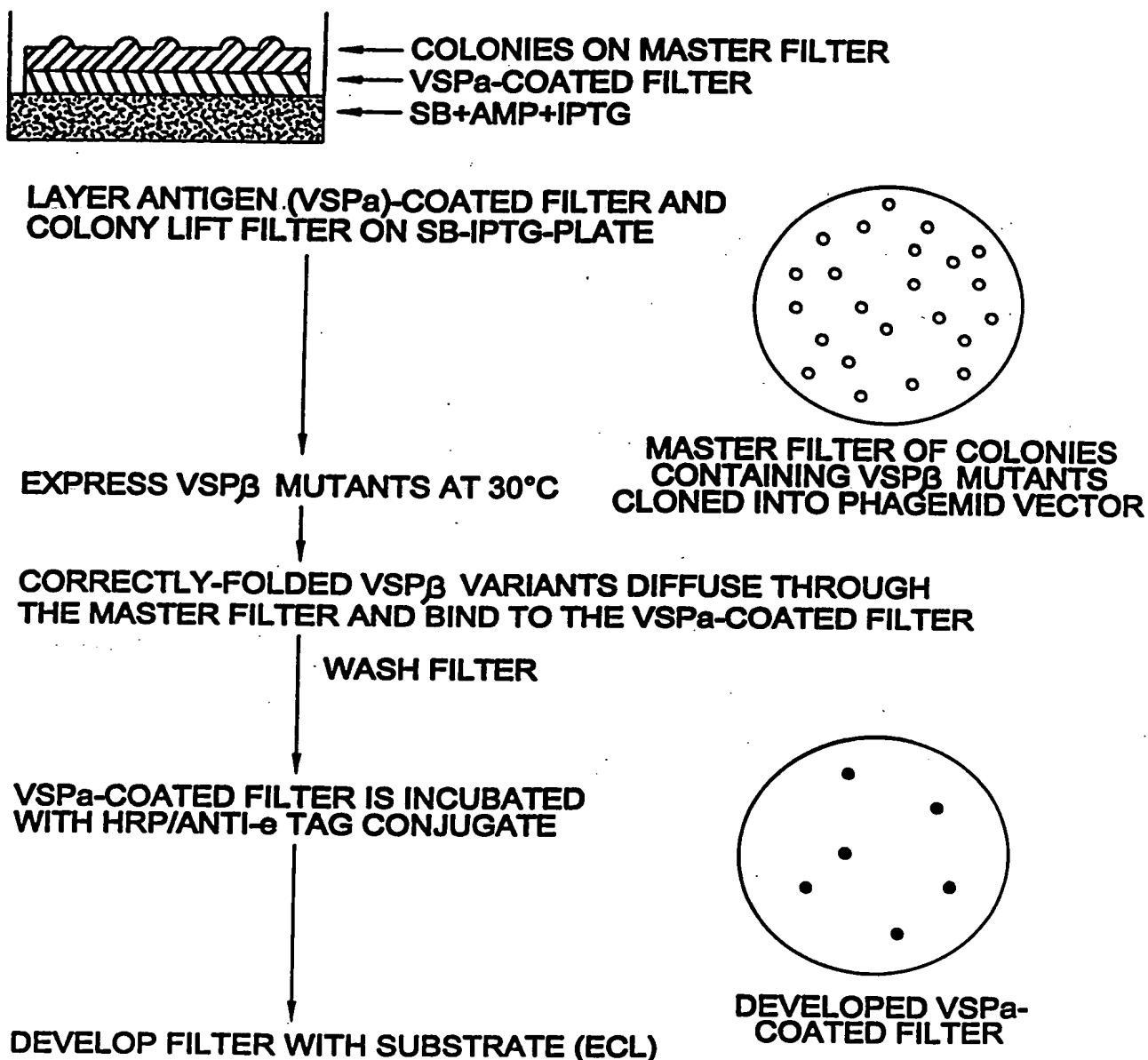


FIG. 5.